Delete paragraph 203, on page 60 and insert the following:

--[**0203**] Mouse genomic DNA was prepared using DNAzol (Gibco/BRL). Blots containing restriction digested DNA (5 μg/lane) were hybridized to a 257-bp 5' probe corresponding to exons 2 and 3 derived from exon trapping (Péterfy *et al.* (1999) *Genomics* 62: 436-444), or a 225-bp 3' probe corresponding to part of the 3' UTR and generated by PCR (5'-TAC GCA GGG ACA CAT TTC CA-3', SEQ ID NO:3) and 5'-GAG AGA TGC AGC TGC GTC A-3', SEQ ID NO:14). Hybridizations were performed at 65°C in 0.5 M sodium phosphate, pH 7.0, 7% SDS, 1% BSA, and washed at 65°C to a final stringency of 0.1X SSC/ 0.1% SDS. Hybridization signals were detected by phosphorimaging.--

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Delete paragraph 205, on pages 60-61 and insert the following:

--[**0205**] PCR amplification of genomic DNA was performed in an M/J Research PTC-200 thermocycler (1 min 94°C, 45 sec 55°C, 1-2 min 72°C) for 30-32 cycles. Primers for amplification of the inversion breakpoints (Fig. 2*b*) were: p1, 5'-CCC TTG AGC ACG TTC ACA-3' (SEQ ID NO:15); p2, 5'-CTG ATC GTT GTC AGT CTC T-3' (SEQ ID NO:16); p3, 5'-GGT TGT GGG GAC CCT GGA-3' (SEQ ID NO: 17); p4, 5'-GCC TGC TGC AGA TGC GTT-3' (SEQ ID NO:18). RACE cloning of full length cDNAs for *Lpin2* and *Lpin3* was performed using liver cDNA template prepared with the Marathon cDNA Amplification Kit (Clontech). PCR products were TA-cloned into pCR2.1 (Invitrogen), and sequenced using the Amplicycle sequencing kit (Perkin Elmer) and an ABI model 373A sequencer.--

A3

Delete paragraph 206, on page 61 and insert the following:

--[**0206**] The entire coding region of the lipin cDNA was amplified from liver cDNA using the primers 5'-GCT CGA ATT CAG ACA ATG AAT TAC GTG GGG CAG CT-3' (SEQ ID NO:19) and 5'-CGT GCA GTC GAC GCT GAG GCT GAA TGC ATG TCC TGG T-3' (SEQ ID NO:20) and cloned as an *Eco*RI/*Sal*I fragment into the pEGFP-N1 vector (Clontech). 3T3-L1 cells were transfected using Lipofectin (Gibco/BRL). 48 hours after transfection, cells were fixed with

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A4 Cont'l

4% paraformaldehyde in PBS, stained with Hoechst-33258 dye, and observed with a Zeiss Axiophot fluorescence microscope.--

Delete paragraph 208 on page 61 and insert the following:

--[**0208**] *Lpin2* and *Lpin3* were mapped using a mouse-hamster radiation hybrid panel (Research Genetics) (McCarthy *et al.* (1997) *Genome Res.* 7: 1153-1161). Oligonucleotide primer pairs derived from the 3'UTR of each gene were as follows: *Lpin2* (5-GGC GAG ACC CAA TCC CTG A-3', SEQ ID NO:21) and 5'-GGG TCT TCC TCT GTA AGA-3', SEQ ID NO:22); *Lpin3* (5'-CCT GGC TTG AGC TTG CCT T-3', SEQ ID NO:23, and 5'-CCC ACG GCA TGC ATC TTC T-3', SEQ ID NO:24).--

A5

Delete paragraph 217 on page 63 and insert the following:

--[**0217**] The N-LIP and acidic lipin protein domains are required for nuclear localization (Figures **Error! Reference source not found.** and **Error! Reference source not found.**). Initial studies of lipin localization within the cell revealed that lipin occurs as a predominantly nuclear protein, with a small, but consistent number of cells that exhibit exclusively cytoplasmic localization. Lipin contains a putative nuclear localization signal (NLS) comprised of basic amino acids (KKRRKRRK, SEQ ID NO:25).--

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In accordance with 37 CFR §1.121 a marked up version of the above-amended paragraph(s) illustrating the changes introduced by the forgoing amendment(s) are provided in Appendix C.

REMARKS

This preliminary amendment is provided in Response to the Notice to File Missing Parts of Nonprovisional Application. Applicant(s) request entry of this amendment in adherence with 37 C.F.R. §§1.821 to 1.825. This amendment is accompanied by a floppy disk containing the sequences (SEQ ID NOs:1-25) in computer readable form, and a paper copy of the sequence information that has been printed from the floppy disk.

The information contained in the computer readable form (floppy disk) was prepared through the use of the software program "PatentIn" and is identical to that of the paper copy.